

APPENDIX A

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1 MSDKKG-VPARELPETPS WAVAVVFAAMVLVSVM EHGLHKLGHWFQHRHKKALWEALEK SEQ ID NO:39
  M:: . PAR.LPETPS WAVA:VFA.M::VSVL: EH:LHKLGHWF:.RHK:AL EALEK Majority
1 MAEDYEYPPARTLPETPS WAVALVFAVMIIVSVLL EHALHKLGHWFHKKRHNALAEALEK SEQ ID NO:32

60 MKAEL MLVGFISSLLIVTQDPPIIAKICI SEDAADVMPCKRGTEGRKPSKYVD-YCP-EG SEQ ID NO:39
  :KAEL MLVGFISSLL VTQDPI : ICI SE.AA.:M:PC. ... K SKY D YC: .G Majority
61 IKAEL MLVGFISSLLAVTQDPISG-ICI SEKAASIMRPCSLPPGSVK-SKYKDYYCAKKG SEQ ID NO:32

118 KVALMSTGSLHQLH VFIFVLAVFHVTYSVITIAL SRLKMRTWKKWETETTSLEYQFANDP SEQ ID NO:39
  KV:LMSTGSLHQLH :FIFVLAVFHVTYSVI.:AL SRLKMRTWKKWETET:SLEYQFANDP Majority
119 KVS LMSTGSLHQLH IFIFVLAVFHVTYSVIIMAL SRLKMRTWKKWETETASLEYQFANDP SEQ ID NO:32

178 ARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSONSK SEQ ID NO:39
  ARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHL:NSK Majority
179 ARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSHNSK SEQ ID NO:32

238 FDFHKYIKRSMEDDFK VVVGISLPLWGVAILTLFL DINGVG TLIWISFIPLVILLCV GTK SEQ ID NO:39
  FDFHKYIKRSMEDDFK VVVGISLPLW VAILTLFL DI:G:G TL.WISFIPLVILLCV GTK Majority
239 FDFHKYIKRSMEDDFK VVVGISLPLWCVAITLFL DIDGIG TLTWISFIPLVILLCV GTK SEQ ID NO:32

298 LEMIIMEMALEIQDRASVIKAPVVEPSNKFFWFHRPDWLFFIHLTLFQNAFQMAHFVW SEQ ID NO:39
  LEMIIMEMALEIQDRASVIKAPVVEPSNKFFWFHRPDWLFFIHLTLFQNAFQMAHFVW Majority
299 LEMIIMEMALEIQDRASVIKAPVVEPSNKFFWFHRPDWLFFIHLTLFQNAFQMAHFVW SEQ ID NO:32

358 TVATPGLKKCYHTQIGLSIMK VVVG LALQFLCSYMTFPLYALV TQMGSNMKRSIFDEQTS SEQ ID NO:39
  TVATPGLKKC:H :IGLSIMK VV:GLALQFLCSY:TFPLYALV TQMGSNMKRSIFDEQT: Majority
359 TVATPGLKKCFMHIGLSIMK VVLGLALQFLCSYITFPLYALV TQMGSNMKRSIFDEQTA SEQ ID NO:32

418 KALTNWRNTAKE KKKVRD TDMLMAQMIGDATPSRGSSPMPSPRGSSPVHLLHKMGMRSDDP SEQ ID NO:39
  KALTNWRNTAKE KKKVRD TDMLMAQMIGDATPSRG:SPMPSPRGSSPVHLLHKMGMRSDDP Majority
419 KALTNWRNTAKE KKKVRD TDMLMAQMIGDATPSRGTSMPSPSRASSPVHLLHKMGMRSDDP SEQ ID NO:32

478 QSAPTSPTQOEARMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG SEQ ID NO:39
  QSAPTSPT :EARMYPVVVAHPVHRLNP.DRRRS.SSSAL:ADIPSADFSFSQG Majority
479 QSAPTSPTMEEARMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADFSFSQG SEQ ID NO:32

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LEGEND: Pairwise alignment of the Mlo amino acid sequences from *Hordeum vulgare* (SEQ ID NO:39, gi:1877221) and wheat (SEQ ID NO:32) was performed using the Lipman-Pearson method found in the Megalign section of the DNASTar suite using the default parameters. The program constructs tables of K-tuples to find regions of similarity. The alignment is then optimized using a trimmed-down version of the Needleman-Wunsch method developed by Lipman and Pearson (*Science* 227:1435-1441). The barley sequence (SEQ ID NO:39) is shown in the first line, the wheat sequence (SEQ ID NO:32) is shown on the third line. The middle line (Majority) displays amino acids that are identical, favorable mismatches represented by colons, neutral mismatches represented by periods, and unfavorable mismatches as spaces. The program uses dashes to maximize the alignment.

Amino acids corresponding to the six membrane-spanning regions and the nuclear localization signal (K-K-K-V-R-D) mentioned on page 699 (Figure 2) of Büschges are written in white and boxed in black. The two casein kinase II motifs located immediately upstream of the nuclear localization signal are underlined.